Package ‘biobtreeR’

January 10, 2024

Type Package
Title Using biobtree tool from R
Version 1.14.0
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Description The biobtreeR package provides an interface to [biobtree](https://github.com/tamerh/biobtree) tool which covers large set of bioinformatics datasets and allows search and chain mappings functionalities.
License MIT + file LICENSE
Encoding UTF-8
LazyLoad yes
NeedsCompilation no
URL https://github.com/tamerh/biobtreeR
BugReports https://github.com/tamerh/biobtreeR/issues
VignetteBuilder knitr
Suggests BiocStyle, knitr, testthat, rmarkdown, markdown
Imports httr, httpuv, stringi, jsonlite, methods, utils
biocViews Annotation
RoxygenNote 6.1.1

git_url https://git.bioconductor.org/packages/biobtreeR
git_branch RELEASE_3_18
git_last_commit b97b014
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-01-10
Description

biobtree covers all the genomes in ensembl and ensembl genomes. If the the studied organism genome is not included in the default pre built in databases then this function is used and build the biobtree database locally for given genomes.

Usage

bbBuildCustomDB(taxonomyIDs = NULL, rawArgs = NULL)

Arguments

taxonomyIDs  Comma seperated list of taxonomy identifiers for building the genomes
rawArgs  For using all available biobtree command line arguments directly

Value

returns empty

Author(s)

Tamer Gur
bbBuiltInDB

Examples

## Not run:

bbUseOutDir("your directory path")
bbBuildCustomDB(taxonomyIDs="1408103,206403")

## End(Not run)

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**bbBuiltInDB**

*Get pre build biointree database*

**Description**

Pre build biointree database for commonly studied datasets and model organism genomes. Once this function called it retrieves the pre build database saves to users output directory.

**Usage**

bbBuiltInDB(type = "1")

**Arguments**

- **type**
  
  built in database type accepted values are 1,2,3 and 4. Currently there are 4 different builtin database; Type 1 Requires ~ 5 GB free storage Included datasets hgnc,hmdb,taxonomy,go,efo,eco,chebi,interpro Included uniprot proteins and ensembl genomes belongs to following organisms
  
  
  Type 2 Requires ~ 5 GB free storage Instead of genomes in the type 1 it contains human and all the mouse strains genomes with their uniprot proteins. In addition hgnc,hmdb,taxonomy,go,efo,eco,chebi,interpro datasets are included
  
  Type 3 Requires ~ 4 GB storage Contains no genome but it contains all the uniprot data with hgnc,hmdb,taxonomy,go,efo,eco,chebi,interpro datasets are included
  
  Type 4 Requires ~ 13 GB storage Contains no genome but full uniprot and chembl data with hgnc,hmdb,taxonomy,go,efo,eco,chebi,interpro

**Value**

returns empty
Author(s)

Tamer Gur

Examples

bbUseOutDir(tempdir()) # temp dir for demo purpose
bbBuiltInDB("demo") # small demo database for real database use 1, 2, 3 or 4

bbConfig-class  

Class for biobtreeR config

Description

This class holds the datasets meta data and web service endpoints and used while executing the search/mapping queries. Instance of this class with name bbConfig is globally set by bbStart function. About dataset meta data, this class instance holds all the datasets unique identifiers, entry url templates etc. In biobtree each dataset has unique character and numeric identifier. For instance Uniprot's character identifier is "uniprot" and numeric identifier is 1. When performing queries the dataset character identifier is used for convinience but in actual database it is saved numerically.

bbEntry  

Retrieve entry

Description

Returns entry for an identifier and dataset. Entry contains all the data raw data for and entry such as mappings, attributes and paging info if exists.

Usage

bbEntry(identifier, source)

Arguments

identifier  
Identifier for the entry. Note that keywords are not accepted. For instance insted of "vav_human" keyword "p15498" identifier must be passed

source  
Dataset identifier

Value

returns biobtree json object
**bbEntryFilter**

**Author(s)**

Tamer Gur

**Examples**

```r
bbStart() # if not already started
bbEntry("HGNC:12009","hgnc")
```

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**bbEntryFilter** Retrieve entry with filtered dataset

**Description**

Similar with entry retrieval but filtered mapping entries with given datasets.

**Usage**

```r
bbEntryFilter(identifier, source, filters, page = NULL)
```

**Arguments**

- `identifier`: Identifier for the entry.
- `source`: Dataset identifier
- `filters`: Comma separated dataset identifier to retrieve
- `page`: Page index if results is more than default biobtree paging size.

**Value**

returns biobtree json object

**Author(s)**

Tamer Gur

**Examples**

```r
bbStart() # if not already started
bbEntryFilter("HGNC:12009","hgnc","uniprot,ensembl")
```
bbEntryPage

Retrieve entry result page

Description

If an entry contains large set of mapping entries it is paginated by biobtree with configured paging size. This function retrieve these paging for an entry. Biobtree paging size for each entry is 200.

Usage

bbEntryPage(identifier, source, page, totalPage)

Arguments

identifier Identifer for the entry.
source Dataset identifier
page Page index it starts from 0
totalPage Total number of page for the entry. This value needs to calculate by user via using total number of entries which is available at the root result for the entry and divide it to the paging size of 200

Value

returns biobtree json object

Author(s)

Tamer Gur

Examples

bbStart() # if not already started
bbEntryPage("ENSG00000141956","ensembl",0,0)
bbListAttrs

**Retrieve attributes of dataset**

**Description**

Provides list of available attributes for a dataset to use in search and mapping queries.

**Usage**

bbListAttrs(dataset)

**Arguments**

- **dataset**
  
  Dataset identifier

**Value**

attributes names

**Examples**

bbListAttrs("hgnc")
bbListAttrs("ensembl")

bbListDatasets

**List available datasets**

**Description**

Lists the available source and target datasets with their numeric identifiers.

**Usage**

bbListDatasets()

**Value**

returns datasets

**Examples**

bbListDatasets()
bbMapping

Chain mapping and filtering

Description

Chain mapping identifiers or keywords with filtering and retrieving attributes if available.

Usage

bbMapping(terms, mapfilter, page = NULL, source = NULL, lite = TRUE, limit = 1000, inattrs = NULL, attrs = NULL, showInputColumn = FALSE)

Arguments

terms
Input terms for the mapping. Same with search functionality they can be comma separated identifiers or keywords

mapfilter
Mapping query which consist of map and optional filter functions in the form of map(dataset).filter(Boolean query expression) The boolean expressions are based on datasets attributes and dataset attributes can be list with bbAttr function. Dataset attributes which used in the filters starts with their dataset name. In biobtree boolean expressions feature has been implemented via Google common expression language so its full capability can be checked in its documentation.

page
Optional parameter works similar with bbSearch page paramter.

source
Optional dataset identifiers for searching input terms within the given dataset.

lite
By default it is TRUE and allow function return quickly with data.frame with mapping identifiers and attributes. If set to TRUE function return raw results converted from json.

limit
Limits the number of mapping results. By default without any limit all the results returned.

inattrs
Optional comma seperated attribute names for input identifiers and if available their values includes in result data.frame

attrs
Optional comma seperated attribute names for mapping identifiers and if available their values includes in result data.frame

showInputColumn
Optional logical parameter to show the input identifiers in the result data.frame

Value

returns mapping results in data.frame by default if lite set it true returns json object

Author(s)

Tamer Gur
Examples

bbStart()

bbMapping("tpi1",'map(uniprot)')

bbMapping("shh",'map(ensembl)')

## Not run:
# run these examples with building the default dataset with bbBuildData()
#Map protein to its go terms and retrieve go term types
bbMapping("AT5G3_HUMAN","map(go),attrs = "type")

#Map protein to its go terms with filter by its type and retrieve their types
bbMapping("AT5G3_HUMAN","map(go).filter(go.type=="biological_process"),attrs = "type")

#Map gene names to exon identifiers and retrieve the region
bbMapping("ATP5MC3,TP53","map(transcript).map(exon),attrs = "seq_region_name")

#Map Affymetrix identifiers to Ensembl identifiers and gene names
bbMapping("202763_at,213596_at,209310_s_at","map(transcript).map(ensembl),attrs = "name")

## End(Not run)

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**bbSearch**

Search identifiers or special keywords

**Description**

Search identifiers or special keywords terms uniformly and resolve their actual unique identifiers and datasets. Keywords can be several things for instance for uniprot an accession like "vav_human" can be a keyword which points to its original identifier "P15498". Or gene name can be also a keyword like "tpi1" which could points multiple dataset like ensembl and hgnc.

**Usage**

```r
bbSearch(terms, source = NULL, filter = NULL, page = NULL,
          limit = 1000, showURL = FALSE, lite = TRUE)
```

**Arguments**

- **terms**: Comma separated identifiers or keywords
- **source**: Optional dataset identifiers to search only within this dataset.
- **filter**: Filter expression useful to filter out results when a keyword point several results. For instance if the biobtree index with multiple organism a same gene search could hit several results for different species to filter only a specific species a filter can apply to search function.
By default no need to pass this parameter since it returns all the results. It can be used with limit parameter for very large results to process them in paginated manner. About paging every long search or mapping result paginated in biobtree and for paginated results every response contains a key to get the next page results. So if this parameter is set with this key specified next page results returned for the given search term.

**limit**
Limits the number of search results. By default without any limit all the results returned.

**showURL** allows returning the dataset source url

**lite** By default it is TRUE and allow function return quickly with data.frame containing most important fields. If set to TRUE function return raw results converted from json.

Value
returns search results in data.frame by default if lite set it true returns json object

Author(s)
Tamer Gur

Examples

bbSearch("hunk,vav_human")

bbSearch("hunk","ensembl",filter='ensembl.genome=="homo_sapiens"')

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bbStart

Start biobtreeR

Description

Once target datasets is built with bbBuildData this function used to start biobtree server in the background for performing search/mapping queries.

Usage

bbStart()

Value

character

Examples

bbStart()
bbStop()
bbStop

Stop biobtree

Description
Stops running background biobtree process which started with bbStart

Usage
bbStop()

Value
returns empty

Examples
bbStop()

bbUseOutDir

Output directory for biobtreeR

Description
Allows to set the directory for the package for its files. It is required to set a valid directory.

Usage
bbUseOutDir(outDir)

Arguments
outDir path for the output directory.

Value
returns empty

Examples
bbUseOutDir(tempdir())
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